

RP INTERACTION WITH PHC2.
RX PubMed=15094067; DOI=10.1016/S0014-5793(04)00351-5;
RA Yannoni Y.M., Gaestel M., Lin L.L.;
RT "P66(ShcA) interacts with MAPKAP kinase 2 and regulates its
RT activity.";
RL FEBS Lett. 564:205-211(2004).
CC -!- FUNCTION: Its physiological substrate seems to be the small heat
CC shock protein (HSP27/HSP25). In vitro can phosphorylate glycogen
CC synthase at Ser-7 and tyrosine hydroxylase (on Ser-19 and Ser-40).
CC This kinase phosphorylates Ser in the peptide sequence, Hyd-X-R-
CC X(2)-S, where Hyd is a large hydrophobic residue (By similarity).
CC -!- ENZYME REGULATION: Seems to be activated by two distinct pathways:
CC the first involves the stimulation of p42/p44 MAPK by growth
CC factors, the second, triggered by stress and heat shock, depends
CC on the activation of MPK2 and upstream MAPKK/MAPKKK.
CC -!- SUBUNIT: Interacts with PHC2.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P49137-1; Sequence=Displayed;
CC Note=Has a nuclear localization signal;
CC Name=2;
CC IsoId=P49137-2; Sequence=VSP 004910;
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined.
CC -!- PTM: Phosphorylated and activated by MAP kinase.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL; U12779; AAA20851.1; -; mRNA.
DR EMBL; BC036060; AAH36060.2; -; mRNA.
DR EMBL; BC052584; AAH52584.1; -; mRNA.
DR EMBL; X75346; CAA53094.1; -; mRNA.
DR PIR; JC2204; JC2204.
DR PIR; S39793; S39793.
DR PDB; 1KWP; X-ray; A/B=1-400.
DR PDB; 1NXK; X-ray; A/B/C/D=1-400.
DR PDB; 1NY3; X-ray; A=1-400.
DR Ensembl; ENSG00000162889; Homo sapiens.
DR HGNC; HGNC:6887; MAPKAPK2.
DR MIM; 602006; gene.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0000165; P:MAPKK cascade; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW 3D-structure; Alternative splicing; ATP-binding; Kinase;
KW Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT CHAIN 1 400 MAP kinase-activated protein kinase 2.
FT /FTid=PRO 000086288.
FT DOMAIN 64 325 protein kinase.
FT NP_BIND 70 78 ATP (By similarity).
FT COMPBIAS 10 40 pro-rich.
FT COMPBIAS 35 40 Poly-Pro.
FT ACT_SITE 186 186 Proton acceptor.
FT BINDING 93 93 ATP (By similarity).
FT MOD_RES 328 328 Phosphoserine (by autocatalysis) (By
FT similarity).
FT 334 334 Phosphothreonine (by MAPK) (By
FT similarity).
FT 354 400 EEMTSALATMRVDYEQIKKIEDASNPLLKRRKKARALE

AAALAH -> GCLHDKNSDOATWLTRL (in isoform
2).
/FTid=VSP 004910.
H -> D (in Ref. 3).
WS -> LV (in Ref. 3).
FT CONFLICT 116 116
FT CONFLICT 247 248
FT HELIX 45 47
FT STRAND 48 50
FT STRAND 55 55
FT STRAND 57 57
FT HELIX 59 61
FT TURN 62 62
FT STRAND 63 73
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FT STRAND 335 335
FT STRAND 337 337
FT HELIX 338 344
SQ SEQUENCE 400 AA; 45568 MW; E4EFFF11CCF288DC CRC64;
Query Match 100.0%; Score 2106; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.1e-115;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQGSPVPFPAPAPPQPPPTPALPHPPAQPPPPPPQPPQFPHVKSGLQIKKNAIDDDYK 60
|||||

12, 65 4 175, 5 SQGSP, 61 0:22

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RESULT 2
QSSY41_HUMAN
ID Q5SY41_HUMAN PRELIMINARY; PRT; 400 AA.
AC QSSY41;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Mitogen-activated protein kinase-activated protein kinase 2.
GN Name=MAPKAPK2; ORFNames=RP11-343H5.3-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Harrison E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Belongs to the Ser/thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AL591846; CA113544.1; -; Genomic_DNA.
DR SMR; Q5SY41; 41-357.
DR Ensembl; ENSG00000162889; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 400 AA; 45568 MW; E4EFFFF1CCF288DC CRC64;

Query Match 100.0%; Score 2106; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.1e-115;

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RESULT 3

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ID MAPK2_MOUSE STANDARD; PRT; 386 AA.

AC P49138; Q6P561;

DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.

DT 04-JAN-2005, sequence version 2.

DT 07-FEB-2006, entry version 47.

DE MAP kinase-activated protein kinase 2 (EC 2.7.1.-) (MAPK-activated

DE protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2).

GN Name=Mapkapk2; Synonyms=Rps6kcl1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] OF 2-386.

RC TISSUE=Lung;

RX MEDLINE=94085571; PubMed=8262198; DOI=10.1016/0014-5793(93)81628-D;

RA Engel K., Plath K., Gaestel M.;

RT "The MAP kinase-activated protein kinase 2 contains a proline-rich

RT SH3-binding domain.";

RL FEBS Lett. 336:143-147(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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AC P49138; Q6P561;

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DT 07-FEB-2006, entry version 47.

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DE protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2).

GN Name=Mapkapk2; Synonyms=Rps6kcl1;

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OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

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RC TISSUE=Lung;

RX MEDLINE=94085571; PubMed=8262198; DOI=10.1016/0014-5793(93)81628-D;

RA Engel K., Plath K., Gaestel M.;

RT "The MAP kinase-activated protein kinase 2 contains a proline-rich

RT SH3-binding domain.";

RL FEBS Lett. 336:143-147(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
D 1231 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
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D 1291 CTGCTGAAACACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
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D 1351 ATCATGCAATCAACAAAGGTCCTCAACCCCACTGCACACCCAGCCGGGTCTTGAAGGAG 1410
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D 1411 GACAAGGAGCGGTGGAGGATGTCAAGGGG 1440

RESULT 8
LOCUS DD182194 1305 bp DNA linear PAT 19-DEC-2005
DEFINITION Methods and Compositions for Protein Expression and Purification.
ACCESSION DD182194
VERSION DD182194.1 GI:83957055
KEYWORDS JP 2005514025-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1305)
AUTHORS Malakhova, O.A., Butt, T.R., Tran, H.T., Malakhov, M.P. and Weeks, S.D.
TITLE Methods and Compositions for Protein Expression and Purification
JOURNAL Patent: JP 2005514025-A 15 19-MAY-2005;
Tauseef Butt, Stephen Weeks, Hiep Tran, Oxana Malakhova, Micheal Malakhov

COMMENT
OS Artificial Sequence
PN JP 2005514025-A/15
PD 19-MAY-2005
PF 07-JAN-2003 JP 2003557532
PI oxana a malakhova, tauseef r butt, hiep t tran, micheal p PI
malakhov,
PI stephen d weeks
CC Synthetic Sequence
FH Key Location/Qualifiers.
1. 1305
/organism="synthetic construct"
/mol_type="unassigned DNA"
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FEATURES
source
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Best Local Similarity 100.0%; Pred. No. 4.8e-256;
Matches 982; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 GCAGTCCACGTCAAGTCCGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAA 179
D 321 GCAGTCCACGTCAAGTCCGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAA 380
QY 180 GGTACACAGCCAGGTCTGGCTGGGTCATCAACGGCAAGTTTTCAGATCTTCAACAA 239
D 381 GGTACACAGCCAGGTCTGGCTGGGTCATCAACGGCAAGTTTTCAGATCTTCAACAA 440
QY 240 GAGGACCCAGGAGAAATTCGCTCAAAATGCTTCAGAGTCCCCCAAGCCCGCAGGGA 299
D 441 GAGGACCCAGGAGAAATTCGCTCAAAATGCTTCAGAGTCCCCCAAGCCCGCAGGGA 500
QY 300 GGTGAGCTGCACCTGGCTCCAGTCCCGGCATCGTACGGATCGTGGATGTGA 359
D 501 GGTGAGCTGCACCTGGCTCCAGTCCCGGCATCGTACGGATCGTGGATGTGA 560
QY 360 CGAGAATCTGTACGAGGAGGAAGTCCCTGCTGATGTATGGAATGTTGGACGGTGG 419

Db 561 CGAGAACTGTACGAGGAGGAGAACTCCCTGCTGATTGTGTCATGGAATGTTTGGACGGTGG 620
QY 420 AGAACTCTTTAGCCGAATCCAGGATCGAGGAGACCCAGGATTCACAGAAAGAGAAGCATC 479
D 621 AGAACTCTTTAGCCGAATCCAGGATCGAGGAGACCCAGGATTCACAGAAAGAGAAGCATC 680
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D 681 CGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCAATCAATCAACATTCGCCA 740
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D 801 ACTCACTGACTTTGGCTTTGCCAAGGAAACCCAGCCACCACTCTTTGACCACTCCTTG 860
QY 660 TTATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAGTATGACAAAGTCTCTG 719
D 861 TTATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAGTATGACAAAGTCTCTG 920
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QY 780 CTCCAACCCAGGCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTA 839
D 981 CTCCAACCCAGGCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTA 1040
QY 840 TGAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAA 899
D 1041 TGAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAA 1100
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QY 960 GATCATGCAATCAACAAAGGTCCCTCAACCCCACTGCACACCCAGCCGGTCTCTGAAGGA 1019
D 1161 GATCATGCAATCAACAAAGGTCCCTCAACCCCACTGCACACCCAGCCGGTCTCTGAAGGA 1220
QY 1020 GGACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTCCCTTGGCCCAATGCG 1079
D 1221 GGACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTCCCTTGGCCCAATGCG 1280
QY 1080 CGTTGACTACGAGCAGATCAAG 1101
D 1281 CGTTGACTACGAGCAGATCAAG 1302

RESULT 9
AY335730
LOCUS AY335730
DEFINITION Synthetic construct Homo sapiens mitogen-activated protein kinase-activated protein kinase 2 (MAPKAPK2) mRNA, partial cds.
ACCESSION AY335730
VERSION AY335730.1 GI:33304098
KEYWORDS FLI CDNA.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1065)
AUTHORS Park, J., Hu, Y., Murthy, T.V.S., Vannberg, F., Shen, B., Rolfs, A., Hutt, J.E., Cantley, L.C., LaBaer, J., Harlow, E. and Brizuela, L.
TITLE Building a human kinase gene repository: Bioinformatics, molecular cloning, and functional validation
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)
PUBMED 15928075
REFERENCE 2 (bases 1 to 1065)
AUTHORS Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E., LaBaer, J. and Brizuela, L.